



0590  
036

## RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/080,114  
Source: OTPE  
Date Processed by STIC: 3-8-2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

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Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



Does Not Comply  
Corrected Diskette Needed

OIIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/080,114 DATE: 03/08/2002  
TIME: 14:17:01

Input Set : A:\EP.txt  
Output Set: N:\CRF3\03082002\J080114.raw

4 <110> APPLICANT: Dhugga, Kanwarpal S.  
5 Niu, Xiaomu  
6 Helentjaris, Timothy  
8 <120> TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes  
9 to Improve Stalk and Grain Quality  
12 <130> FILE REFERENCE: 1301  
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/080,114  
C--> 14 <141> CURRENT FILING DATE: 2002-02-21  
14 <150> PRIOR APPLICATION NUMBER: 60/270,777  
15 <151> PRIOR FILING DATE: 2001-02-22  
17 <160> NUMBER OF SEQ ID NOS: 13  
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

# ERRORED SEQUENCES

21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 2737  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Zea mays  
26 <400> SEQUENCE: 1

*number needs to be moved to right hand margin*

E--> 27 gtcgaccac ggcgtccggcg accgcgtcga ggacaccctc cagcgcacc gcaacgagct  
W--> 28 60gtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atcctgcagc cgcaccacat  
W--> 29 120cctcgacgcg ctgcagcagg tccagggtc cggggggcgc gcgctagccg agggaccctt  
W--> 30 180ctcgacgtc ctccgctccg cgcaggaggc gatcgtgctg ccgcggttcg tggccatcgc  
W--> 31 240gtgctgccc cgcgccggag tttgggagta cgtccgcgtc aacgttcacg agctcagcgt  
W--> 32 300cgagcagctc acagtctcgg agtacctccg cttcaaggag gagcttgctg acggccagca  
W--> 33 360aatgatccc tacgttctcg agcttgaact cgagccgttc aatgtctcag tcccacgccc  
W--> 34 420aaatcggtca tcatctattg gaaacggtgt gcagttcctc aaccgacact tgtcctcaat  
W--> 35 480catgttccgc aacagggatt gcttgaggcc cctgttggtt ttcctccgtg gccaccggca  
W--> 36 540caaggggcat gttatgatgc ttaatgatag aatacaaaagc ttggggaggc ttcagtctgt  
W--> 37 600ctgaccaa gctgaggagc acttgtcaaa gctccctgct gacacacat actcacaatt  
W--> 38 660tgcttataaa tttcaagagt ggggcctgga gaaaggttgg ggtgatacag caggacatgt  
W--> 39 720tttggaatg atccatctcc ttctagacat cattcaggcg ccagacccat ctaccctaga  
W--> 40 780gaaattcttg gggaggatcc ccatgatttt taacgttggt gtggtatccc ctcatggata  
W--> 41 840cttttggtcaa gctaatgtat taggcttgcc agacacagga ggacagatcg tctatatact  
W--> 42 900ggaaccaagtc cgtgcactag aaaatgagat ggttctccgt ttaaagaaac aagggttga  
W--> 43 960gttttcccca aagattctca ttgttactcg gctgatacca gatgcaaaag gaacatcatg  
W--> 44 1020aatcagcgg cttgagagaa ttagtggaac acagcatact tacatattac gagttccctt  
W--> 45 1080agaaatgaa aatgggatac ttaagaaatg gatatcaaga tttgatgtgt ggcataatct  
W--> 46 1140ggaacattt gctgaggatg ctgctggtga aattgctgct gaattacaag gtactccaga  
W--> 47 1200cttcataaatt ggaaactaca gtgatggaaa tcttggtggcgc tcattgctat cttacaagat  
W--> 48 1260gggaattacc cagtgaaca ttgctcatgc tctggaaaag actaagtatc cagattcaga

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Input Set : A:\EP.txt

Input Set: N:\CRF3\03082002\J080114.raw

W--> 49 1320 catatttttg aagaatttcg atgagaagta ccattttctc tgccagtcca ctgctgatat  
W--> 50 1380 aattgctatg aacaatgctg attttatcat caccagcaca taccaagaaa ttgctggaag  
W--> 51 1440 caaaaatact gttggacagt atgagagtca tactgccttt actctgcctg gtctgtaccg  
W--> 52 1500 agttgtccat gggatcgatg tcttcgatcc aaagtccaat atagtctctc ctggagctga  
W--> 53 1560 catgtccata tactttccac ataccgagaa ggccaagcga ctcacctctc ttcattggttc  
W--> 54 1620 aatcgaaaat ttgatttatg acccgagca aaacgatgaa cacattgggc atctggatga  
W--> 55 1680 ccggtcaaag cccatcctct tctccatggc aagactcgac aggggtgaaga acataacagg  
W--> 56 1740 gctggtcgaa gcttttgcta agtgcgctaa gctgagggag ctggtaaacc ttgtcgtcgt  
W--> 57 1800 tgcgggttac aatgatgtca acaagtccaa ggacagggaa gagatcgagg agatagagaa  
W--> 58 1860 gatgcatgaa ctcatcaaga cccacaactt gtcggggcag ttcgctgga tctctgccca  
W--> 59 1920 gacaaacagg gcccgtaacg gcgagctcta tcgctacatc gctgataccc atgggtgcttt  
W--> 60 1980 cgtacagccg gccttgtagt aagcgttcgg tctcaccgtc gttgaggcca tgacctgtgg  
W--> 61 2040 gcttcctact ttccgcagcg tccatggagg tccagctgag atcatagagc atggcgtctc  
W--> 62 2100 gggtctccac attgacctg accaccccca acaggctgtt aatctgatgg ccgacttctt  
W--> 63 2160 gacgggtgc aagcaagacc cagatcactg ggtgaatata tctggagcag ggctgcagcg  
W--> 64 2220 catatacgag aagtacacat ggaagatata ctcagagagg ttgatgacac tggccggggg  
W--> 65 2280 ctacggtttc tggaagtacg tgcgaagct cgagaggctg gagacgaggc gctaccttga  
W--> 66 2340 gatgtttctac atactgaagt tccgcgagct ggcgaagacc gtgccgcttg caattgacca  
W--> 67 2400 accgcagtag cttgcgcaac tgcgactgcg tagcacttgg tacaagactg aaacctgaag  
W--> 68 2460 gaccttcagt aatttaggcg cggcagacgg tagccaataa aatgtgccgg agctgaactg  
W--> 69 2520 gttttttatt atgtacataa tggcagtata acaaaattac tgaaggcagg tgggttcgag  
W--> 70 2580 ttgtgtgttc gttactgttt actgtattat gtcaagctgt cggtgcaat ttctttgctg  
W--> 71 2640 gcaagccgca ggcactggtg aagtgtgat aaatacatca tattctgttg acctgtgaaa  
E--> 72 2700 aaaaaaaaaa aaaaaaaaaa aaaaaaggg cgggccgc

74 <210> SEQ ID NO: 2

75 <211> LENGTH: 802

76 <212> TYPE: PRT

77 <213> ORGANISM: Zea mays

79 <400> SEQUENCE: 2

80 Ser Thr His Ala Ser Gly Asp Arg Val Glu Asp Thr Leu His Ala His I  
E--> 81 5 10 15 Arg Asn Glu Leu Val Ala Leu Leu  
82 Ser Lys Tyr Val Asn Lys Gly Lys 20  
E--> 83 30 Gly Ile Leu Gln Pro His His Ile Leu Asp Ala Leu Asp Glu Val Gln  
E--> 84 35 40 45 Gly Ser Gly Gly Arg Ala  
85 Leu Ala Glu Gly Pro Phe Leu Asp Val Leu 50 55  
E--> 86 60 Arg Ser Ala Gln Glu Ala Ile Val Leu Pro Pro Phe Val Ala Ile  
E--> 87 Ala65 70 75 80 Val Arg Pro  
88 Arg Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val His 85  
E--> 89 90 95 Glu Leu Ser Val Glu Gln Leu Thr Val Ser Glu Tyr Leu  
E--> 90 Arg Phe Lys 100 105 110 Glu  
91 Glu Leu Val Asp Gly Gln His Asn Asp Pro Tyr Val Leu Glu Leu 115  
E--> 92 120 125 Asp Phe Glu Pro Phe Asn Val Ser Val Pro Arg  
93 Pro Asn Arg Ser Ser 130 135 140  
94 Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Ile145  
E--> 95 150 155 160 Met Phe Arg Asn Arg Asp Cys Leu Glu  
96 Pro Leu Leu Asp Phe Leu Arg 165 170  
E--> 97 175 Gly His Arg His Lys Gly His Val Met Met Leu Asn Asp Arg Ile Gln  
E--> 98 180 185 190 Ser Leu Gly Arg Leu Gln Ser  
99 Val Leu Thr Lys Ala Glu Glu His Leu 195 200

2737

this is correct location  
for nucleotide numbering

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

Major format error in  
Amino acid sequences. USE MAX  
of 16 amino acids per line with  
numbering under every 5th amino acid 3/8/02

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/080,114

DATE: 03/08/2002

TIME: 14:17:01

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

*see page 2*

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E--> 100 205          Ser Lys Leu Pro Ala Asp Thr Pro Tyr Ser Gln Phe Ala Tyr Lys Phe
E--> 101 210          215          220          Gln Glu Trp Gly Leu
      102 Glu Lys Gly Trp Gly Asp Thr Ala Gly His Val225          230
E--> 103 235          240 Leu Glu Met Ile His Leu Leu Leu Asp Ile Ile Gln Ala Pro
E--> 104 Asp Pro          245          250          255          Ser Thr
      105 Leu Glu Lys Phe Leu Gly Arg Ile Pro Met Ile Phe Asn Val          260
E--> 106 265          270          Val Val Val Ser Pro His Gly Tyr Phe Gly Gln Ala
      107 Asn Val Leu Gly          275          280          285
      108 Leu Pro Asp Thr Gly Gly Gln Ile Val Tyr Ile Leu Asp Gln Val Arg          290
E--> 109 295          300          Ala Leu Glu Asn Glu Met Val Leu Arg Leu
      110 Lys Lys Gln Gly Leu Asp305          310          315
E--> 111 320 Val Ser Pro Lys Ile Leu Ile Val Thr Arg Leu Ile Pro Asp Ala Lys
E--> 112 325          330          335          Gly Thr Ser Cys Asn Gln Arg Leu
      113 Glu Arg Ile Ser Gly Thr Gln His          340          345
E--> 114 350          Thr Tyr Ile Leu Arg Val Pro Phe Arg Asn Glu Asn Gly Ile Leu Lys
E--> 115 355          360          365          Lys Trp Ile Ser Arg Phe
      116 Asp Val Trp Pro Tyr Leu Glu Thr Phe Ala          370          375
E--> 117 380          Glu Asp Ala Ala Gly Glu Ile Ala Ala Glu Leu Gln Gly Thr Pro
E--> 118 Asp385          390          395          400 Phe Ile Ile
      119 Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu          405
E--> 120 410          415          Ser Tyr Lys Met Gly Ile Thr Gln Cys Asn Ile Ala His
E--> 121 Ala Leu Glu          420          425          430          Lys
      122 Thr Lys Tyr Pro Asp Ser Asp Ile Phe Trp Lys Asn Phe Asp Glu          435
E--> 123 440          445          Lys Tyr His Phe Ser Cys Gln Phe Thr Ala Asp
      124 Ile Ile Ala Met Asn          450          455          460
      125 Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser465
E--> 126 470          475          480 Lys Asn Thr Val Gly Gln Tyr Glu Ser
      127 His Thr Ala Phe Thr Leu Pro          485          490
E--> 128 495          Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe
E--> 129 500          505          510          Asn Ile Val Ser Pro Gly Ala
      130 Asp Met Ser Ile Tyr Phe Pro His Thr          515          520
E--> 131 525          Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu
E--> 132 530          535          540          Ile Tyr Asp Pro Glu
      133 Gln Asn Asp Glu His Ile Gly His Leu Asp Asp545          550
E--> 134 555          560 Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg
E--> 135 Val Lys          565          570          575          Asn Ile
      136 Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg          580
E--> 137 585          590          Glu Leu Val Asn Leu Val Val Val Ala Gly Tyr Asn
      138 Asp Val Asn Lys          595          600          605
      139 Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu          610
E--> 140 615          620          Ile Lys Thr His Asn Leu Phe Gly Gln Phe
      141 Arg Trp Ile Ser Ala Gln625          630          635
E--> 142 640 Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr
E--> 143 645          650          655          His Gly Ala Phe Val Gln Pro Ala
      144 Leu Tyr Glu Ala Phe Gly Leu Thr          660          665
E--> 145 670          Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His
E--> 146 675          680          685          Gly Gly Pro Ala Glu Ile
      147 Ile Glu His Gly Val Ser Gly Phe His Ile          690          695
E--> 148 700          Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe

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E--> 149 Phe705 710 715 720 Asp Arg Cys  
 150 Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala 725  
 E--> 151 730 735 Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile  
 E--> 152 Tyr Ser Glu 740 745 750 Arg  
 153 Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser 755  
 E--> 154 760 765 Lys Leu Glu Arg Leu Glu Thr Arg Arg Tyr Leu  
 155 Glu Met Phe Tyr Ile 770 775 780  
 156 Leu Lys Phe Arg Glu Leu Ala Lys Thr Val Pro Leu Ala Ile Asp Gln785  
 E--> 157 790 795 800 Pro Gln  
 392 <210> SEQ ID NO: 5  
 393 <211> LENGTH: 802  
 394 <212> TYPE: PRT  
 395 <213> ORGANISM: Zea mays  
 397 <400> SEQUENCE: 5  
 398 Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly 1  
 E--> 399 5 10 15 Ala Thr Phe Ser Ser His Pro Asn  
 400 Glu Leu Ile Ala Leu Phe Ser Arg 20 25  
 E--> 401 30 Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Ala  
 E--> 402 35 40 45 Glu Phe Asp Ala Leu Phe  
 403 Asp Ser Asp Lys Glu Lys Tyr Ala Pro Phe 50 55  
 E--> 404 60 Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro  
 E--> 405 Trp65 70 75 80 Val Ala Leu  
 406 Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg 85  
 E--> 407 90 95 Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val  
 E--> 408 Ser Glu Tyr 100 105 110 Leu  
 409 Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn Ser Asn Phe 115  
 E--> 410 120 125 Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala  
 411 Ser Phe Pro Arg Pro 130 135 140  
 412 Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His145  
 E--> 413 150 155 160 Leu Ser Ser Lys Leu Phe Gln Asp Lys  
 414 Glu Ser Leu Tyr Pro Leu Leu 165 170  
 E--> 415 175 Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met Met Leu Asn  
 E--> 416 180 185 190 Asp Arg Ile Gln Ser Leu Arg  
 417 Gly Leu Gln Ser Ser Leu Arg Lys Ala 195 200  
 E--> 418 205 Glu Glu Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr Ser Glu Phe  
 E--> 419 210 215 220 Asn His Arg Phe Gln  
 420 Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr225 230  
 E--> 421 235 240 Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp Leu  
 E--> 422 Leu Glu 245 250 255 Ala Pro  
 423 Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr Ile Pro Met 260  
 E--> 424 265 270 Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr  
 425 Phe Ala Gln Ser 275 280 285  
 426 Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu 290  
 E--> 427 295 300 Asp Gln Val Arg Ala Leu Glu Asn Glu Met  
 428 Leu Leu Arg Ile Lys Gln305 310 315  
 E--> 429 320 Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu  
 E--> 430 325 330 335 Pro Asp Ala Ala Gly Thr Thr Cys  
 431 Gly Gln Arg Leu Glu Lys Val Ile 340 345  
 E--> 432 350 Gly Thr Glu His Thr Asp Ile Ile Arg Val Pro Phe Arg Asn Glu Asn

See page 2

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E--> 433 355          360          365          Gly Ile Leu Arg Lys Trp
      434 Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu          370          375
E--> 435 380          Glu Thr Tyr Thr Glu Asp Val Ser Ser Glu Ile Met Lys Glu Met
E--> 436 Gln385          390          395          400 Ala Lys Pro
      437 Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val          405
E--> 438 410          415          Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys
E--> 439 Thr Ile Ala          420          425          430          His
      440 Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp          435
E--> 441 440          445          Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln
      442 Phe Thr Ala Asp Leu          450          455          460
      443 Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu465
E--> 444 470          475          480 Ile Ala Gly Ser Lys Asp Thr Val Gly
      445 Gln Tyr Glu Ser His Ile Ala          485          490
E--> 446 495          Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
E--> 447 500          505          510          Asp Pro Lys Phe Asn Ile Val
      448 Ser Pro Gly Ala Asp Met Ser Val Tyr          515          520
E--> 449 525          Tyr Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
E--> 450 530          535          540          Ile Glu Glu Leu Ile
      451 Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe545          550
E--> 452 555          560 Val Leu Lys Asp Lys Lys Lys Pro Ile Ile Phe Ser Met Ala
E--> 453 Arg Leu          565          570          575          Asp Arg
      454 Val Lys Asn Met Thr Gly Leu Val Glu Met Tyr Gly Lys Asn          580
E--> 455 585          590          Ala Arg Leu Arg Glu Leu Ala Asn Leu Val Ile Val
      456 Ala Gly Asp His          595          600          605
      457 Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Lys Met          610
E--> 458 615          620          Tyr Ser Leu Ile Asp Glu Tyr Lys Leu Lys
      459 Gly His Ile Arg Trp Ile625          630          635
E--> 460 640 Ser Ala Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr Arg Tyr Ile
E--> 461 645          650          655          Cys Asp Thr Lys Gly Ala Phe Val
      462 Gln Pro Ala Phe Tyr Glu Ala Phe          660          665
E--> 463 670          Gly Leu Thr Val Ile Glu Ser Met Thr Cys Gly Leu Pro Thr Ile Ala
E--> 464 675          680          685          Thr Cys His Gly Gly Pro
      465 Ala Glu Ile Ile Val Asp Gly Val Ser Gly          690          695
E--> 466 700          Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu
E--> 467 Val705          710          715          720 Asn Phe Phe
      468 Asp Lys Cys Lys Ala Asp Pro Ser Tyr Trp Asp Glu Ile          725
E--> 469 730          735          Ser Gln Gly Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr
E--> 470 Trp Lys Leu          740          745          750          Tyr
      471 Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys          755
E--> 472 760          765          Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg
      473 Arg Tyr Ile Glu Met          770          775          780
      474 Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ser Gln Val Pro Leu Ser785
E--> 475 790          795          800 Phe Asp
      703 <210> SEQ ID NO: 7
      704 <211> LENGTH: 816
      705 <212> TYPE: PRT
      706 <213> ORGANISM: Zea mays
      708 <400> SEQUENCE: 7
      709 Met Gly Glu Gly Ala Gly Asp Arg Val Leu Ser Arg Leu His Ser Val 1

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```

E--> 710 5          10          15      Arg Glu Arg Ile Gly Asp Ser Leu
      711 Ser Ala His Pro Asn Glu Leu Val          20          25
E--> 712 30      Ala Val Phe Thr Arg Leu Lys Asn Leu Gly Lys Gly Met Leu Gln Pro
E--> 713 35          40          45          His Gln Ile Ile Ala Glu
      714 Tyr Asn Asn Ala Ile Pro Glu Ala Glu Arg          50          55
E--> 715 60          Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala
E--> 716 Gln65          70          75          80 Glu Ala Ile
      717 Val Ile Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg          85
E--> 718 90          95      Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu
E--> 719 Leu Ala Val          100          105          110          Glu
      720 Glu Leu Arg Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val          115
E--> 721 120          125          Glu Glu Gly Pro Asn Asn Asn Phe Val Leu Glu
      722 Leu Asp Phe Glu Pro          130          135          140
      723 Phe Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn145
E--> 724 150          155          160 Gly Val Gln Phe Leu Asn Arg His Leu
      725 Ser Ser Lys Leu Phe His Asp          165          170
E--> 726 175      Lys Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr
E--> 727 180          185          190          Lys Gly Met Thr Met Met Leu
      728 Asn Asp Arg Ile Arg Ser Leu Ser Ala          195          200
E--> 729 205          Leu Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Thr Leu Gln
E--> 730 210          215          220          Ala Asp Thr Pro Tyr
      731 Ser Glu Phe His His Arg Phe Gln Glu Leu Gly225          230
E--> 732 235          240 Leu Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu
E--> 733 Thr Ile          245          250          255          His Leu
      734 Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu          260
E--> 735 265          270          Lys Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val
      736 Val Ile Leu Ser          275          280          285
      737 Pro His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr          290
E--> 738 295          300          Gly Gly Gln Val Val Tyr Ile Leu Asp Gln
      739 Val Arg Ala Met Glu Asn305          310          315
E--> 740 320 Glu Met Leu Leu Arg Ile Lys Gln Cys Gly Leu Asp Ile Thr Pro Lys
E--> 741 325          330          335          Ile Leu Ile Val Thr Arg Leu Leu
      742 Pro Asp Ala Thr Gly Thr Thr Cys          340          345
E--> 743 350      Gly Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Cys His Ile Leu
E--> 744 355          360          365          Arg Val Pro Phe Arg Thr
      745 Glu Asn Gly Ile Val Arg Lys Trp Ile Ser          370          375
E--> 746 380      Arg Phe Glu Val Trp Pro Tyr Leu Glu Thr Tyr Thr Asp Asp Val
E--> 747 Ala385          390          395          400 His Glu Ile
      748 Ala Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly          405
E--> 749 410          415      Asn Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala
E--> 750 His Lys Met          420          425          430          Gly
      751 Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr          435
E--> 752 440          445          Pro Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu
      753 Asp His Tyr His Phe          450          455          460
      754 Ser Cys Gln Phe Thr Thr Asp Leu Ile Ala Met Asn His Ala Asp Phe465
E--> 755 470          475          480 Ile Ile Thr Ser Thr Phe Gln Glu Ile
      756 Ala Gly Asn Lys Asp Thr Val          485          490
E--> 757 495      Gly Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg
E--> 758 500          505          510          Val Val His Gly Ile Asp Val

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/080,114

DATE: 03/08/2002

TIME: 14:17:01

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

*See page 2*

```

      759 Phe Asp Pro Lys Phe Asn Ile Val Ser          515          520
E--> 760 525          Pro Gly Ala Asp Leu Ser Ile Tyr Phe Pro Tyr Thr Glu Ser His Lys
E--> 761 530          535          540          Arg Leu Thr Ser Leu
      762 His Pro Glu Ile Glu Glu Leu Leu Tyr Ser Gln545          550
E--> 763 555          560 Thr Glu Asn Thr Glu His Lys Phe Val Leu Asn Asp Arg Asn
E--> 764 Lys Pro          565          570          575          Ile Ile
      765 Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly          580
E--> 766 585          590          Leu Val Glu Leu Tyr Gly Arg Asn Lys Arg Leu Gln
      767 Glu Leu Val Asn          595          600          605
      768 Leu Val Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu          610
E--> 769 615          620          Glu Gln Ala Glu Phe Lys Lys Met Phe Asp
      770 Leu Ile Glu Gln Tyr Asn625          630          635
E--> 771 640 Leu Asn Gly His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg
E--> 772 645          650          655          Asn Gly Glu Leu Tyr Arg Tyr Ile
      773 Cys Asp Thr Lys Gly Ala Phe Val          660          665
E--> 774 670          Gln Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met
E--> 775 675          680          685          Thr Cys Gly Leu Pro Thr
      776 Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu          690          695
E--> 777 700          Ile Ile Val His Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln
E--> 778 Gly705          710          715          720 Asp Lys Ala
      779 Ser Ala Leu Leu Val Asp Phe Phe Asp Lys Cys Gln Ala          725
E--> 780 730          735          Glu Pro Ser His Trp Ser Lys Ile Ser Gln Gly Gly Leu
E--> 781 Gln Arg Ile          740          745          750          Glu
      782 Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu          755
E--> 783 760          765          Thr Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser
      784 Asn Leu Glu Arg Arg          770          775          780
      785 Glu Thr Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Thr785
E--> 786 790          795          800 Met Ala Ser Thr Val Pro Leu Ala Val
      787 Glu Gly Glu Pro Ser Ser Lys          805          810
E--> 788 815

```



## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/080,114

DATE: 03/08/2002

TIME: 14:17:02

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:27 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1  
L:28 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:29 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:29 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:30 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:30 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:31 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:31 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:32 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:33 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:33 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:34 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:35 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:36 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:37 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:37 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:38 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:39 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:40 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:42 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:43 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:44 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:46 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:48 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:50 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/080,114

DATE: 03/08/2002

TIME: 14:17:02

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:51 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:52 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:52 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:54 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:55 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:56 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:57 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:58 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:59 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:60 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:62 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:63 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:64 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:66 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:67 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:68 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:69 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:70 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:71 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 M:254 Repeated in SeqNo=1  
 L:72 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4  
 L:72 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2737 Found:97 SEQ:1  
 L:81 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:83 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
 L:83 M:333 E: Wrong sequence grouping, Amino acids not in groups!

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/080,114

DATE: 03/08/2002

TIME: 14:17:02

Input Set : A:\EP.txt

Output Set: N:\CRF3\03082002\J080114.raw

M:332 Repeated in SeqNo=2

L:84 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:86 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:87 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:87 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:89 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:118 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:118 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:149 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:149 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:157 M:252 E: No. of Seq. differs, <211>LENGTH:Input:802 Found:451 SEQ:2  
L:399 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:401 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5  
L:401 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
M:332 Repeated in SeqNo=5

L:402 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:404 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:405 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:405 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:407 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:436 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:436 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:467 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:467 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:475 M:252 E: No. of Seq. differs, <211>LENGTH:Input:802 Found:451 SEQ:5  
L:710 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:712 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:712 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
M:332 Repeated in SeqNo=7

L:713 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:715 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:716 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:716 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:718 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:747 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:747 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:778 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:778 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:788 M:252 E: No. of Seq. differs, <211>LENGTH:Input:816 Found:458 SEQ:7